SEQUENCE LISTING

<110> van Rooijen, Gijs
      Keon, Richard Glenn
      Boothe, Joseph
      Shen, Yin

<120> Commercial Production of Chymosin in Plants

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1               5                   10                  15

caa tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct     96
Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
            20                  25                  30

ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt    144
Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
        35                  40                  45

cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac    192
Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
    50                  55                  60

tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat    240
Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
65                  70                  75                  80

agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc    288
Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
                85                  90                  95

acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc    336
Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
            100                 105                 110

tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga    384
Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
        115                 120                 125

aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac    432
Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
    130                 135                 140

ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc    480
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Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
145             150             155             160

tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa    528
Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
                165             170             175

cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg    576
Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
                180             185             190

gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac    624
Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
            195             200             205

atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg    672
Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
        210             215             220

gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca    720
Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
225             230             235             240

tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag    768
Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
                245             250             255

tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt    816
Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
                260             265             270

gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag    864
Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
            275             280             285

ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga    912
Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
        290             295             300

gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt    960
Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
305             310             315             320

agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca   1008
Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
                325             330             335

ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt   1056
Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
                340             345             350

gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg   1104
Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
            355             360             365

ttc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt   1152
Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
        370             375             380

ggg cta gct aaa gca atc tga                                        1173
Gly Leu Ala Lys Ala Ile
385             390
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Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
            20                  25                  30

Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
        35                  40                  45

Leu Glu Asp Phe Leu Gln Lys Gln Tyr Gly Ile Ser Ser Lys Tyr
    50                  55                  60

Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
65                  70                  75                  80

Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
            85                  90                  95

Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
            100                 105                 110

Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
        115                 120                 125

Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
    130                 135                 140

Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
145                 150                 155                 160

Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
                165                 170                 175

Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
            180                 185                 190

Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
        195                 200                 205

Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
    210                 215                 220

Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
225                 230                 235                 240

Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
            245                 250                 255

Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
            260                 265                 270

Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
        275                 280                 285

Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
        290                 295                 300

Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
305                 310                 315                 320

Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
            325                 330                 335

Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
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            340                    345                    350
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Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
        355                    360                    365
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Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
        370                    375                    380
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Gly Leu Ala Lys Ala Ile
385                    390
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ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga  180

tatccctaca aattattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc  240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt  300

agcgttggta gaaagcataa agatttattc ttattcttct tcatataaat gtttaatata  360

caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat  420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa  480

aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact  540

agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga  600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct  660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat  720

cttctaaagt aatttttaata atagttacta tattcaagat ttcatatatc aaatactcaa  780

tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt  840

aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat  900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac  960

tataacattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020

atgtaagtcc gtaactagaa ttacagtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatgggt cttgcgcaag aaaaagacaa agaacaaaga aaaaagacaa aacagagaga 1140

caaaacgcaa tcacacaacc aactcaaatt agtcactggc tgatcaagat cgccgcgtcc 1200

atgtatgtct aaatgccatg caaagcaaca cgtgcttaac atgcacttta aatggctcac 1260
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ccatctcaac ccacacacaa acacattgcc tttttcttca tcatcaccac aaccacctgt 1320

atatattcat tctcttccgc cacctcaatt tcttcacttc aacacacgtc aacctgcata 1380

tgcgtgtcat cccatgccca aatctccatg catgttccaa ccaccttctc tcttatataa 1440

tacctataaa tacctctaat atcactcact tctttcatca tccatccatc cagagtacta 1500

ctactctact actataatac cccaacccaa ctcatattca atactactct act atg   1556
                                                              Met
                                                               1

aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa   1604
Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln
         5   10   15

tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct ctc   1652
Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu
        20   25   30

tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta   1700
Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu
        35   40   45

gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc   1748
Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser
50   55   60   65

ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt   1796
Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser
                70   75   80

caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc   1844
Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr
                    85   90   95

gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac   1892
Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr
            100   105   110

tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag   1940
Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys
        115   120   125

tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt   1988
Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly
130   135   140   145

aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc   2036
Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser
                150   155   160

aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca   2084
Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro
            165   170   175

ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca   2132
Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala
            180   185   190

tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac atg   2180
Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met
        195   200   205

atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg gac   2228
Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp
210   215   220   225

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agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca tcc   2276
Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser
                230                 235                 240

tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac   2324
Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr
                245                 250                 255

tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt gca   2372
Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala
                260                 265                 270

tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg   2420
Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu
        275                 280                 285

gtc gga cct agc agc gac att ctc aac att cag caa gct att gga gcc   2468
Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala
290                 295                 300                 305

aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt agc   2516
Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser
                310                 315                 320

tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca ctg   2564
Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu
                325                 330                 335

acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt gga   2612
Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly
                340                 345                 350

ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg ttc   2660
Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe
        355                 360                 365

att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt ggg   2708
Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly
370                 375                 380                 385

cta gct aaa gca atc tga agcttaataa gtatgaacta aaatgcatgt         2756
Leu Ala Lys Ala Ile
                390
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tatctatgca ccttattgtt ctatgataaa tttcctctta ttattataaa tcatctgaat 2936

cgtgacggct tatggaatgc ttcaaatagt acaaaaacaa atgtgtacta taagactttc 2996

taaacaattc taactttagc attgtgaacg agacataagt gttaagaaga cataacaatt 3056

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aggatgttaa ggagacataa caattataaa gagagaagtt tgtatccatt tatatattat 3176

atactaccca tttatatatt atacttatcc acttatttaa tgtctttata aggtttgatc 3236

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actctgtata aaggttggat catccttaaa gtgggtctat ttaattttat tgcttcttac 3356

agataaaaaa aaaattatga gttggtttga taaaatattg aaggatttaa aataataata 3416

aataataaat aacatataat atatgtatat aaatttatta taatataaca tttatctata 3476
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gtgtgtccca atccttatac aaccaacttc cacaggaagg tcaggtcggg gacaacaaaa 3716

aaacaggcaa gggaaatttt ttaatttggg ttgtcttgtt tgctgcataa tttatgcagt 3776

aaaacactac acataaccct tttagcagta gagcaatggt tgaccgtgtg cttagcttct 3836

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            20                  25                  30

Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
        35                  40                  45

Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
    50                  55                  60

Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
65                  70                  75                  80

Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
                85                  90                  95

Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
            100                 105                 110

Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
        115                 120                 125

Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
    130                 135                 140

Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
145                 150                 155                 160

Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
                165                 170                 175

Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
            180                 185                 190

Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
        195                 200                 205

Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
210                 215                 220
```

```
Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
225             230         235             240

Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
            245         250             255

Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
        260         265             270

Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
    275         280             285

Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
    290         295             300

Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
305             310             315                 320

Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
            325             330             335

Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
            340         345             350

Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
        355             360             365

Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
    370         375             380

Gly Leu Ala Lys Ala Ile
385             390
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